AMENDMENTS TO THE CLAIMS:

Amend the claims as follows:

- (Currently Amended) A computer assisted method of providing a
 personalized lifestyle advice plan for a human subject comprising:
- (i) providing a first dataset on a data processing device, said first dataset comprising information correlating the presence of individual alleles at genetic loci, wherein at least one allele of each genetic locus known to be associated with increased or decreased disease susceptibility, with a lifestyle risk factor;
- (ii) providing a second dataset on a data processing device, said second dataset comprising information matching each said risk factor with at least one lifestyle recommendation;
- (III) inputting a third dataset identifying alleles present in said subject, wherein said alleles are at one or more of the genetic locialleles of said first dataset; of said human subject;
- (Iv) determining the risk factors associated with said alleles present in said human subject by correlating said alleles with risk factors provided by said first dataset;
- (v) determining at least one lifestyle recommendation based on each identified risk factor from step (iv) by matching said risk factor with a lifestyle recommendation from said second dataset; and
- (vi) generating a personalized lifestyle advice plan based comprising at least one lifestyle recommendation determined in step (v), wherein said personalized lifestyle advice plan includes recommended minimum and/or maximum amounts of food subtypes.

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Claim 2. (Cancelled)

- 3. (Currently Amended) The method according to claim 1 er claim 2-wherein the method comprises the step of delivering the report to the client.
- 4. (Original) The method according to claim 3 wherein the plan is delivered via the Internet and accessible via a unique identifier code.
- (Original) The method according to claim 4 wherein the plan comprises
 hyperlinks to one or more Web pages.
- 6. (Currently Amended) The method according to claim 1 wherein said first dataset comprises information relating to two or more alleles of <u>a gene</u> one or more genetic loci of genes-selected from the group comprising:
- (a) <u>a gene[[s]]</u> that encode<u>s an</u> enzyme[[s]] responsible for detoxification of xenobiotics in Phase I metabolism;
- (b) <u>a gene[[s]]</u> that encode<u>s an</u> enzyme[[s]] responsible for conjugation reactions in Phase II metabolism;
- (c) <u>a gene[[s]]</u> that encode<u>s an</u> enzyme[[s]] that help<u>s</u> cells to combat oxidative stress;
 - (d) a gene[[s]] associated with micronutrient deficiency; and
 - (e) <u>a gene[[s]]</u> that encodes an enzyme[[s]] responsible for metabolism of

alcohol.

- (f) <u>a gene[[s]]</u> that encode<u>s an</u> enzyme[[s]] involved in lipid and/or cholesterol metabolism:
 - (g) a gene[[s]] that encodes an enzyme[[s]] involved in clotting;
 - (h) a gene[[s]] that encodes a trypsin inhibitor[[s]];

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- (i) <u>a gene[[s]]</u> that encode<u>s an</u> enzyme[[s]] related to susceptibility to metal toxicity;
- (j) <u>a gene[[s]]</u> which encode<u>s a protein[[s]]</u> required for normal cellular metabolism and growth;
 - (k) a gene[[s]] which encodes a HLA Class 2 molecule[[s]].
- 7. (Currently Amended) The method according to claim 6 wherein said first dataset comprises information relating to two or more alleles of <u>a gene</u> one or more genetic loci of genes selected from each member of the group comprising:
- (a) <u>a gene[[s]]</u> that encode<u>s an</u> enzyme[[s]] responsible for detoxification of xenobiotics in Phase I metabolism;
- (b) <u>a gene[[s]]</u> that encode<u>s an</u> enzyme[[s]] responsible for conjugation reactions in Phase II metabolism;
- (c) <u>a gene[[s]]</u> that encode<u>s an</u> enzyme[[s]] that help<u>s</u> cells to combat oxidative stress:
 - (d) a gene[[s]] associated with micronutrient deficiency; and
- (e) <u>a gene[[s]]</u> that encode<u>s an</u> enzyme[[s]] responsible for metabolism of alcohol.

- (f) <u>a gene[[s]]</u> that encode<u>s an</u> enzyme[[s]] involved in lipid and/or cholesterol metabolism;
 - (g) a gene[[s]] that encodes an enzyme[[s]] involved in clotting;
 - (h) a gene[[s]] that encodes a trypsin inhibitor[[s]];
- (i) <u>a gene[[s]]</u> that encode<u>s an</u> enzyme[[s]] related to susceptibility to metal toxicity;
- (j) <u>a gene[[s]]</u> which encode<u>s a protein[[s]]</u> required for normal cellular metabolism and growth;
 - (k) a gene[[s]] which encodes a HLA Class 2 molecule[[s]].
- 8. (Currently Amended) The method according to claim 6 wherein said first dataset comprises information relating to two or more alleles of one or more genetic loci of a gene[[s]] encoding an enzyme selected from the group comprising: cytochrome P450 monooxygenase, N-acetyltransferase 1, N-acetyltransferase 2, glutathione-S-transferase, manganese superoxide dismutase, 5,10-methylenetetrahydrofolatereductase and alcohol dehydrogenase 2.
- 9. (Currently Amended) The method according to claim 8 wherein said first dataset comprises information relating to two or more alleles of one or more genetic loci of-each of the genes encoding cytochrome P450 monooxygenase, N-acetyltransferase 1, N-acetyltransferase 2, glutathione-S-transferase, manganese superoxide dismutase, 5,10-methylene-tetrahydrofolatereductase and alcohol dehydrogenase 2.

- 10. (Currently Amended) The method according to claim 1 including the step determining the presence of individual alleles at one or more genetic loci of the DNA in a DNA sample of said human subject, and constructing the dataset used in step (iii) using results of said determination.
- 11. (Original) The method according to claim 10 wherein said presence of said individual alleles is determined by hybridisation with allele-specific oligonucleotides.
- 12. (Original) The method according to claim 11 wherein said allele specific oligonucleotides are selected from oligonucleotides each specific for one of the genes selected from the group comprising the CYP1A1 gene, the GST μ gene, the GST μ gene, the GST θ gene, the NAT1 gene, the NAT2 gene, the MnSOD gene, the MTHFR gene and the ALDH2 gene.
- 13. (Previously Presented) The method of claim 9 wherein said alleles are alleles of genes selected from the group consisting of the MTHFR gene, the MnSOD gene, the CYP1A1 gene, the GST μ gene, GST π gene, the GST θ gene and the ALDH2 gene.
- 14. (Currently Amended) A computer assisted method of providing a personalized lifestyle advice plan for a human subject comprising:
- (i) providing a first dataset on a data processing device, said first dataset comprising information correlating the presence of individual alleles at genetic loci,

wherein at least one allele of each genetic locus known to be associated with increased or decreased disease susceptibility, with a lifestyle risk factor;

- (ii) providing a second dataset on a data processing device, said second dataset comprising information matching each said risk factor with at least one lifestyle recommendation;
- (iii) inputting a third dataset identifying alleles present in said subject, wherein said alleles are at two or more of the genetic locialleles of said firstdataset of said human subject;
- (iv) determining the risk factors associated with said alleles present in said human subject by correlating said alleles with risk factors provided by said first dataset;
- (v) determining at least one lifestyle recommendation based on each identified risk factor from step (iv) by matching said risk factor with a lifestyle recommendation from said second dataset; and
- (vi) generating a personalized lifestyle advice plan based comprising at least one lifestyle recommendation determined in step (v), wherein said personalized lifestyle advice plan includes recommended minimum and/or maximum amounts of food subtypes.

Claim 15. (Canceled)

16. (Currently Amended) The method according to claim 14 or claim 15 wherein the method comprises the step of delivering the report to the client.

- (Previously Presented) The method according to claim 16 wherein the 17. plan is delivered via the Internet and accessible via a unique identifier code.
- (Previously Presented) The method according to claim 17 wherein the 18. plan comprises hyperlinks to one or more Web pages.
- 19.(Currently Amended) The method according to claim 14 wherein said first dataset comprises information relating to two or more alleles of two or more genetic loci of genes selected from the group comprising:
- (a) a gene[[s]] that encodes an enzyme[[s]] responsible for detoxification of xenobiotics in Phase I metabolism:
- (b) a gene[[s]] that encodes an enzyme[[s]] responsible for conjugation reactions in Phase II metabolism:
- (c) a gene[[s]] that encodes an enzyme[[s]] that help cells to combat oxidative stress:
 - (d) a gene[[s]] associated with micronutrient deficiency; and
- (e) a gene[[s]] that encodes an enzyme[[s]] responsible for metabolism of alcohol.
- (f) a gene[[s]] that encodes an enzyme[[s]] involved in lipid and/or cholesterol metabolism:
 - (g) a gene[[s]] that encodes an enzyme[[s]] involved in clotting;
 - (h) a gene[[s]] that encodes a trypsin inhibitor[[s]];
 - (i) a gene[[s]] that encodes an enzyme[[s]] related to susceptibility to metal

toxicity;

- (j) <u>a gene[[s]]</u> which encode<u>s a protein[[s]]</u> required for normal cellular metabolism and growth;
 - (k) a gene[[s]] which encodes a HLA Class 2 molecule[[s]].
- 20. (Currently Amended) The method according to claim 19 wherein said first dataset comprises information relating to two or more alleles of two or more genetic loci of genesa gene selected from each member of the group comprising:
- (a) <u>a gene[[s]]</u> that encode<u>s an</u> enzyme[[s]] responsible for detoxification of xenobiotics in Phase I metabolism;
- (b) <u>a gene[[s]]</u> that encode<u>s an</u> enzyme[[s]] responsible for conjugation reactions in Phase II metabolism;
- (c) <u>a gene[[s]]</u> that encode<u>s an</u> enzyme[[s]] that help cells to combat oxidative stress:
 - (d) a_gene[[s]] associated with micronutrient deficiency; and
- (e) <u>a gene[[s]]</u> that encode<u>s an</u> enzyme[[s]] responsible for metabolism of alcohol.
- (f) <u>a gene[[s]]</u> that encode<u>s an</u> enzyme[[s]] involved in lipid and/or cholesterol metabolism;
 - (g) a gene[[s]] that encodes an enzyme[[s]] involved in clotting;
 - (h) a gene[[s]] that encodes a trypsin inhibitor[[s]];
- (i) <u>a gene[[s]]</u> that encode<u>s an</u> enzyme[[s]] related to susceptibility to metal toxicity;

- (j) <u>a gene[[s]]</u> which encode<u>s a protein[[s]]</u> required for normal cellular metabolism and growth;
 - (k) a gene[[s]] which encodes a HLA Class 2 molecule[[s]].
- 21. (Currently Amended) The method according to claim 19 wherein said first dataset comprises information relating to two or more alleles of two or more genetic loci of a gene[[s]] encoding an enzyme selected from the group comprising: cytochrome P450 monooxygenase, N-acetyltransferase 1, N-acetyltransferase 2, glutathione-S-transferase, manganese superoxide dismutase, 5,10-methylenetetrahydrofolatereductase and alcohol dehydrogenase 2.
- 22. (Currently Amended) The method according to claim 21 wherein said first dataset comprises information relating to two or more alleles of two or more genetic loci ef-each of the genes encoding cytochrome P450 monooxygenase, N-acetyltransferase 1, N-acetyltransferase 2, glutathione-S-transferase, manganese superoxide dismutase, 5,10-methylenetetrahydrofolatereductase and alcohol dehydrogenase 2.
- 23. (Currently Amended) The method according to claim 14 including the step determining the presence of individual alleles at two or more genetic loci of the DNA in a DNA sample of said human subject, and constructing the dataset used in step (iii) using results of said determination.
 - 24. (Previously Presented) The method according to claim 23 wherein said

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presence of said individual alleles is determined by hybridisation with allele-specific oligonucleotides.

- 25. (Previously Presented) The method according to claim 24 wherein said allele specific oligonucleotides are selected from oligonucleotides each specific for two of the genes selected from the group comprising the CYP1A1 gene, the GST μ gene, the GST μ gene, the NAT1 gene, the NAT2 gene, the MnSOD gene, the MTHFR gene and the ALDH2 gene.
- 26. (Previously Presented) The method of claim 22 wherein said alleles are alleles of genes selected from the group consisting of the MTHFR gene, the MnSOD gene, the CYP1A1 gene, the GSTμ gene, GSTπ gene, the GSTΘθgene and the ALDH2 gene.
- 27. (Previously Presented) The method of claim 1 wherein said first dataset and said second dataset are provided on the same data processing device.
- 28. (Previously Presented) The method of claim 14 wherein said first dataset and said second dataset and provided on the same data processing device.